

Serial Number: 09/671,953

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#10

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number input by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 16 and 17 - moved <2237 response up one line

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/671,953

DATE: 10/10/2001
TIME: 13:44:04

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10102001\I671953.raw

PS

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3 <110> APPLICANT: Meares, Claude
4     Chmura, Albert
5     The Regents of the University of California
7 <120> TITLE OF INVENTION: Engineering Antibodies That Bind Irreversibly
9 <130> FILE REFERENCE: 023070-099120US
11 <140> CURRENT APPLICATION NUMBER: US 09/671,953
12 <141> CURRENT FILING DATE: 2000-09-27
14 <150> PRIOR APPLICATION NUMBER: US 60/156,194
15 <151> PRIOR FILING DATE: 1999-09-27
17 <150> PRIOR APPLICATION NUMBER: US 60/208,684
18 <151> PRIOR FILING DATE: 2000-05-31
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 753
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
31     that encodes Fab heavy chain of CHA255
33 <400> SEQUENCE: 1
34 agatctgaag tgacgctggt ggagtctagg ggagactcag tgaagcctgg agggttcctg 60
35 aaactctcct gtgcagcctc tggattcact ttaagtgggtg aaaccatgtc ttgggttcgc 120
36 cagactccgg agaagaggct ggagtgggtc acaaccactc ttagtggtgg tggtttcacc 180
37 ttctattcag ccagtgtgaa gggtcgtttc accatctcca gagacaatgc ccagaacaac 240
38 ctctatctac aactgaatag tctgaggtct gaggacacgg ccttgtattt ctgtgcaagt 300
39 catcggtttg ttactggggg ccacgggact ctggtcactg tctctgcagc caaaacgacg 360
40 ggcccatcgg tcttccccct ggcacctcc tccaagagca cctctggggg cacagcggcc 420
41 ctgggctgcc tggtaagga ctacttcccc gaaccggtga cgggtgcgtg gaactcaggc 480
42 gccctgacca gcggcgtgca caccctcccg gctgtcctac agtcctcaag actctacttc 540
43 ctgagcagcg tggtgaccgt gcccttcaac agcttgggca cccagacctc catctgcaac 600
44 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag cagagcccaa atcttgtgac 660
45 aaatctagag ggcccttcga aggtaagcct atccctaacc ctctcctcgg tctcgattct 720
46 acgcgtaccg gtcacatca ccatcacat tga 753
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 657
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
56     that encodes light chain mutant with Cys
57     substituted for Asn at position 97 of CHA255
59 <400> SEQUENCE: 2
60 agatctgctg ttgtgactca ggaatctgca ctccaccat cacctggtga aacagtcaca 60
61 ctcaactgtc gctcaagtat tggggctggt acaactagta actatgcaa ctgggtccaa 120
62 gaaaaaccag atcatttatt cactggtcta atagggtgta ccaataaccg ggctccgggt 180
63 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacagg 240

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64 gcacagactg aagatgaggc aagatatattc tgtgctctat ggtactcctg cctctgggtr 300
65 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
66 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
67 aataacttct atcccagaga ggccaaagta cagtgaaggg tggataacgc cctccaatcg 480
68 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
69 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
70 acccatcagg gctgagtyty gcccgtcaca aagagcttca acaggggaga gtgttaa 657
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 657
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
80 that encodes the unmodified light chain of CHA255
82 <400> SEQUENCE: 3
83 agatctgctg ttgtgactca ggaatctgca ctaccacat cacctgggtga aacagtcaca 60
84 ctacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
85 gaaaaaccag atcatttatt cactggtcta atagggtgta ccaataaccg ggctccgggt 180
86 gttcctgccg gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
87 gcacagactg aagatgaggc aagatatattc tgtgctctat ggtactccaa cctctgggtr 300
88 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
89 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
90 aataacttct atcccagaga ggccaaagta cagtgaaggg tggataacgc cctccaatcg 480
91 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
92 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
93 acccatcagg gctgagtyty gcccgtcaca aagagcttca acaggggaga gtgttaa 657
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 657
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
103 that encodes light chain mutant with Cys
104 substituted for Ser at position 96 of CHA255
106 <400> SEQUENCE: 4
107 agatctgctg ttgtgactca ggaatctgca ctaccacat cacctgggtga aacagtcaca 60
108 ctacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
109 gaaaaaccag atcatttatt cactggtcta atagggtgta ccaataaccg ggctccgggt 180
110 gttcctgccg gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
111 gcacagactg aagatgaggc aagatatattc tgtgctctat ggtactgcaa cctctgggtr 300
112 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
113 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
114 aataacttct atcccagaga ggccaaagta cagtgaaggg tggataacgc cctccaatcg 480
115 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
116 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
117 acccatcagg gctgagtyty gcccgtcaca aagagcttca acaggggaga gtgttaa 657
120 <210> SEQ ID NO: 5
121 <211> LENGTH: 218
122 <212> TYPE: PRT

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123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
127     sequence of mutant light chain with Cys
128     substituted for Asn at position 97 of CHA255
130 <220> FEATURE:
131 <221> NAME/KEY: MOD_RES
132 <222> LOCATION: (207)
133 <223> OTHER INFORMATION: Xaa = any amino acid
135 <400> SEQUENCE: 5
136 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
137   1             5             10             15
139 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
140             20             25             30
142 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
143             35             40             45
145 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
146             50             55             60
148 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
149   65             70             75             80
151 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
152             85             90             95
154 Cys Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
155             100            105            110
157 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
158             115            120            125
160 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
161             130            135            140
163 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
164   145            150            155            160
166 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
167             165            170            175
169 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
170             180            185            190
172 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
173             195            200            205
175 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
176             210            215
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 218
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
186     sequence of unmodified light chain of CHA255
188 <220> FEATURE:
189 <221> NAME/KEY: MOD_RES
190 <222> LOCATION: (207)
191 <223> OTHER INFORMATION: Xaa = any amino acid

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Input Set : A:\PTO.AMC.txt

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193 <400> SEQUENCE: 6

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194 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
195   1           5           10           15
197 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
198           20           25           30
200 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
201           35           40           45
203 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
204           50           55           60
206 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
207   65           70           75           80
209 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
210           85           90           95
212 Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
213           100          105          110
215 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
216           115          120          125
218 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
219           130          135          140
221 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
222 145           150          155          160
224 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
225           165          170          175
227 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
228           180          185          190
230 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
231           195          200          205
233 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
234           210          215

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237 <210> SEQ ID NO: 7

238 <211> LENGTH: 218

239 <212> TYPE: PRT

240 <213> ORGANISM: Artificial Sequence

242 <220> FEATURE:

243 <223> OTHER INFORMATION: Description of Artificial Sequence: polypeptide

244 sequence of mutant light chain with Cys

245 substituted for Ser at position 96 of CHA255

247 <220> FEATURE:

248 <221> NAME/KEY: MOD_RES

249 <222> LOCATION: (207)

250 <223> OTHER INFORMATION: Xaa = any amino acid

252 <400> SEQUENCE: 7

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253 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
254   1           5           10           15
256 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
257           20           25           30
259 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
260           35           40           45
262 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg

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Input Set : A:\PTO.AMC.txt

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263      50      55      60
265 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
266 65      70      75      80
268 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Cys
269      85      90      95
271 Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
272      100      105      110
274 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
275      115      120      125
277 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
278      130      135      140
280 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
281 145      150      155      160
283 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
284      165      170      175
286 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
287      180      185      190
289 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
290      195      200      205
292 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
293      210      215
296 <210> SEQ ID NO: 8
297 <211> LENGTH: 250
298 <212> TYPE: PRT
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: polypeptide
303      sequence of unmodified heavy chain of CHA255
305 <400> SEQUENCE: 8
306 Arg Ser Glu Val Thr Leu Val Glu Ser Arg Gly Asp Ser Val Lys Pro
307 1      5      10      15
309 Gly Gly Phe Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
310      20      25      30
312 Gly Glu Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu
313      35      40      45
315 Trp Val Thr Thr Thr Leu Ser Gly Gly Gly Phe Thr Phe Tyr Ser Ala
316      50      55      60
318 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Asn
319 65      70      75      80
321 Leu Tyr Leu Gln Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr
322      85      90      95
324 Phe Cys Ala Ser His Arg Phe Val His Trp Gly His Gly Thr Leu Val
325      100      105      110
327 Thr Val Ser Ala Ala Lys Thr Thr Gly Pro Ser Val Phe Pro Leu Ala
328      115      120      125
330 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
331      130      135      140
333 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
334 145      150      155      160

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 10/10/2001

PATENT APPLICATION: US/09/671,953

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10102001\I671953.raw

L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20